

IV. AMENDMENTS TO THE CLAIMS

1-8. (Canceled)

9. (Currently Amended) A process for the ~~fermentative of~~ production of an L-amino acid, ~~in particular lysine, which comprises carrying out the following steps comprising:~~

a) ~~fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the sigE gene or nucleotide sequence which code for it are enhanced, in particular overexpressed~~ culturing a coryneform bacterium under conditions suitable for overexpression of the sigE gene having the nucleic acid sequence as set forth in SEQ ID NO: 1 and encoding a polypeptide having an amino acid sequence as set forth in SEQ ID NO: 2;

b) ~~concentration of L-amino acid in the medium or in the cells of the bacteria, and enriching the medium or the cells of the bacterium;~~

c) ~~isolation of the~~ isolating the L-amino acid.

10. (Canceled)

11. (Canceled)

12. (Currently Amended) A process ~~as claimed in~~ according to claim 9, wherein a ~~strain~~ said bacteria have been transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the sigE gene which comprises the nucleotide sequence of SEQ ID NO: 1.

13. (Currently Amended) A process as claimed in claim 9, wherein ~~the expression of the polynucleotide(s) which code(s) for the sigE gene is enhanced, in particular overexpressed~~ said overexpression is achieved by increasing the copy number of the sigE gene.

14. (Canceled)

15. (Currently Amended) A ~~The process as claimed in~~ according to claim 9, ~~wherein the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of~~ wherein in a *C. glutamicum* strain, one or more of the genes selected from the group is overexpressed:

- ~~15.1~~ (a) the dapA gene which codes for dihydrodipicolinate synthase,
- ~~15.2~~ (b) the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
- ~~15.3~~ (c) the tpi gene which codes for triose phosphate isomerase,
- ~~15.4~~ (d) the pgk gene which codes for 3-phosphoglycerate kinase,
- ~~15.5~~ (e) the zwf gene which codes for glucose 6-phosphate dehydrogenase,
- ~~15.6~~ (f) the pyc gene which codes for pyruvate carboxylase,
- ~~15.7~~ (g) the mqo gene which codes for malate-quinone oxidoreductase,
- ~~15.8~~ (h) the lysC gene which codes for ~~feed-back resistant~~ aspartate kinase,
- ~~15.9~~ (i) the lysE gene ~~which codes~~ coding for a protein for lysine export,
- ~~15.10~~ (j) the hom gene which codes for homoserine dehydrogenase,
- ~~15.11~~ (j) the ilvA gene which codes for threonine dehydratase ~~or the ilvA(Fbr) allele which codes for a feed-back resistant threonine dehydratase,~~
- ~~15.12~~ (k) the ilvBN gene which codes for acetohydroxy-acid synthase,
- ~~15.13~~ (l) the ilvD gene which codes for dihydroxy-acid dehydratase, and
- ~~15.14~~ (m) the zwal gene which codes for the Zwal protein,

~~is or are enhanced or over-expressed are fermented.~~

16. (Currently Amended) A process as claimed in claim 9, wherein ~~for the preparation of L-amino acids, coryneform microorganisms in which at the same time one or more of the genes chosen from the group consisting of~~ in a *C. glutamicum* strain, one or more of the genes selected from the following group is deleted:

- ~~16.1~~ (a) the pck gene which codes for phosphoenol pyruvate carboxykinase,
- ~~16.2~~ (b) the pgi gene which codes for glucose 6-phosphate isomerase,

- ~~16.3~~ (c) the poxB gene which codes for pyruvate oxidase, and
- ~~16.4~~ (d) the zwa2 gene which codes for the Zwa2 protein.
- ~~is or are attenuated are fermented.~~
17. (Canceled)
18. (Currently Amended) A process as ~~claimed in one or more of the preceding claims, wherein microorganisms of the genus Corynebacterium are employed~~ according to claim 9, wherein said coryneform bacteria are of the species *Corynebacterium glutamicum*.
19. (Canceled)
20. (Canceled)
21. (New) The process according to claim 9, wherein said L-amino acid is L-lysine.
22. (New) The process according to claim 9, wherein said nucleotide sequence comprises nucleotides 302 to 949 of SEQ ID NO: 1.
23. (New) A process for producing L-amino acids comprising:
- a) transforming a coryneform bacterium with a vector which includes a sigE gene having the polynucleotide sequence of SEQ ID NO: 1, wherein said sigE gene is under control of a promoter which allows the overexpression of said sigE gene;
 - b) culturing said bacterium in a medium suitable for expression of the sigE gene to thereby produce L-amino acids; and
 - c) isolating the L-amino acids.
24. (New) A method for the preparation of L-amino acids, comprising:
- culturing coryneform bacteria, which include an overexpressed sigE gene having a polynucleotide sequence which encodes the amino acid sequence of SEQ ID NO: 2, in a medium suitable for the expression of sigE to thereby produce L-amino acids.
25. (New) The method according to claim 24, further comprising isolating the L-amino acids.
26. (New) The method according to claim 24, wherein the bacteria have been transformed with a plasmid vector which comprises the nucleotide sequence of SEQ ID NO: 1.
27. (New) The method according to claim 24, wherein the coryneform bacteria bacteria produce L-lysine.

28. (New) A method according to claim 24, wherein the bacteria are *Corynebacterium glutamicum*.